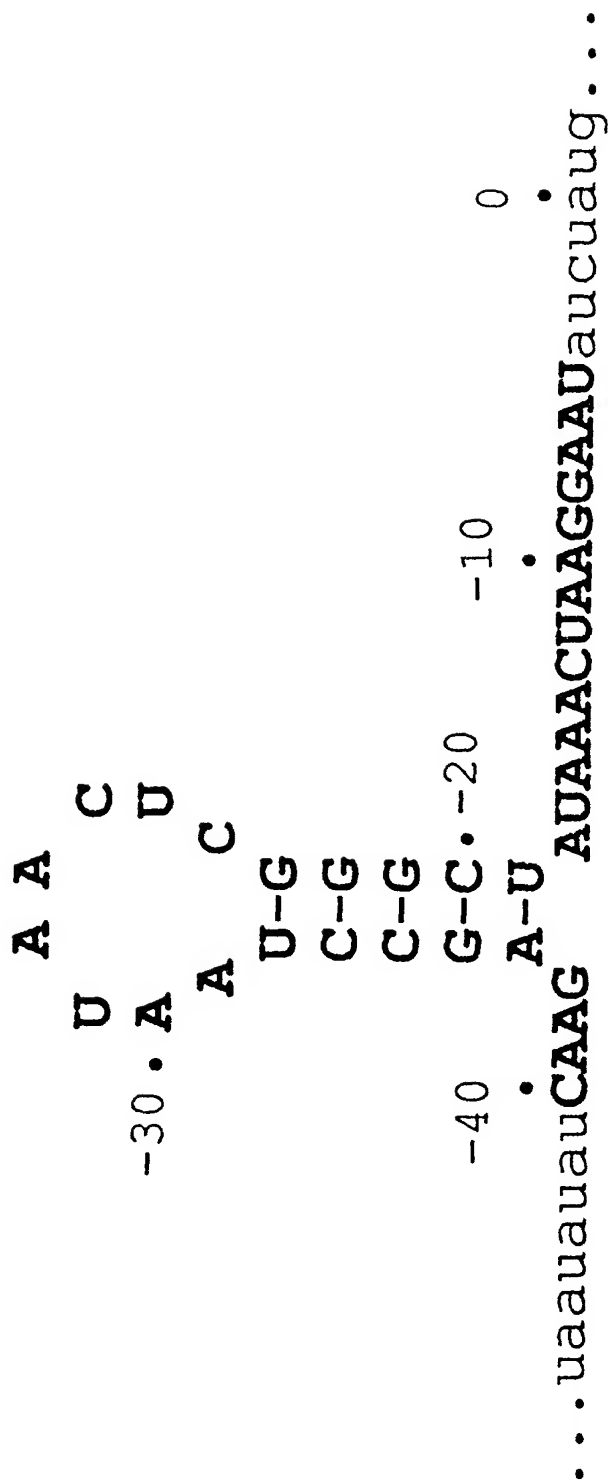


FIG. 1

FIG. 1



SEQ. I.D. NO. 345

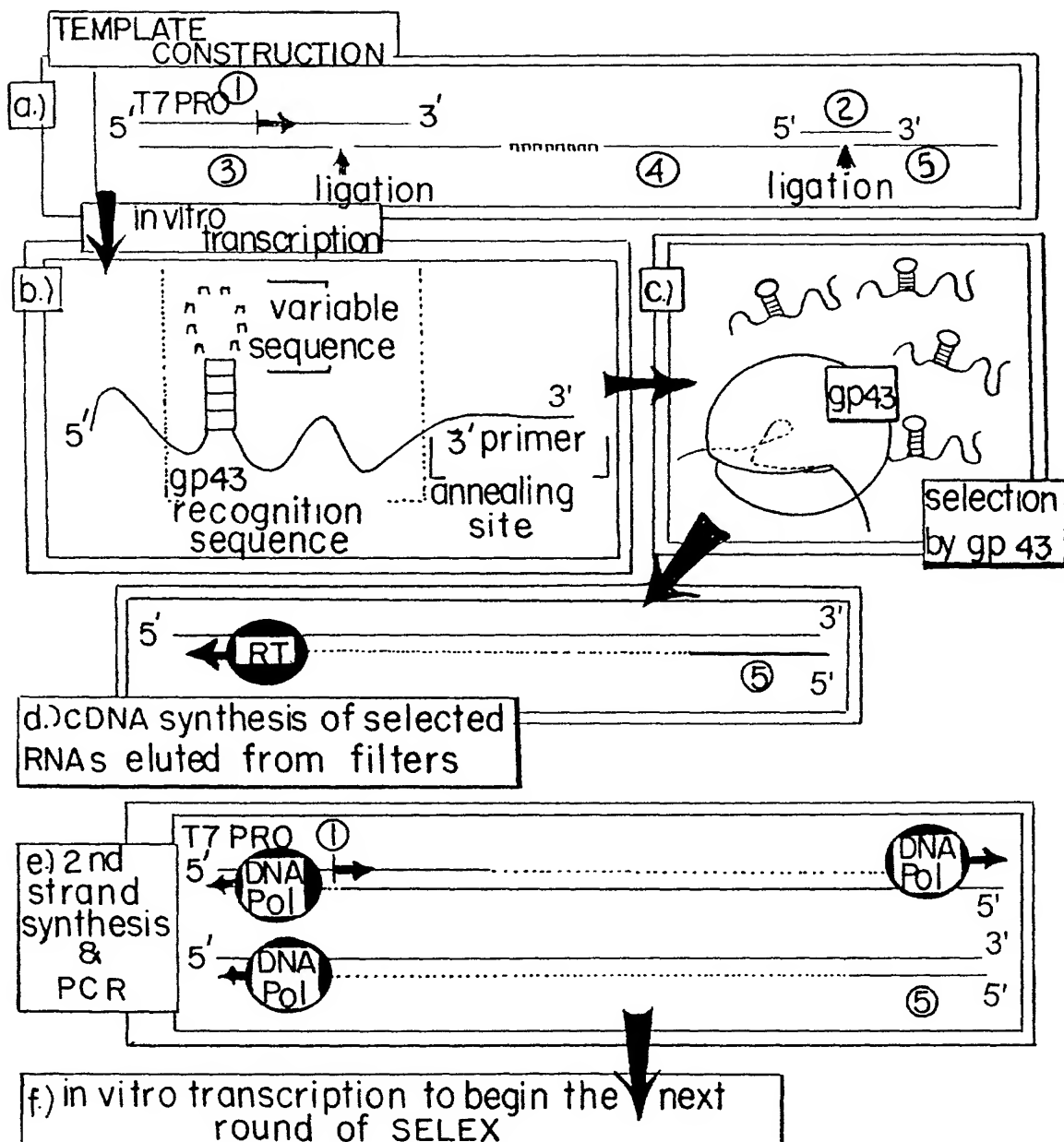


FIG.2

FIG. 3

SELECTION CYCLE:

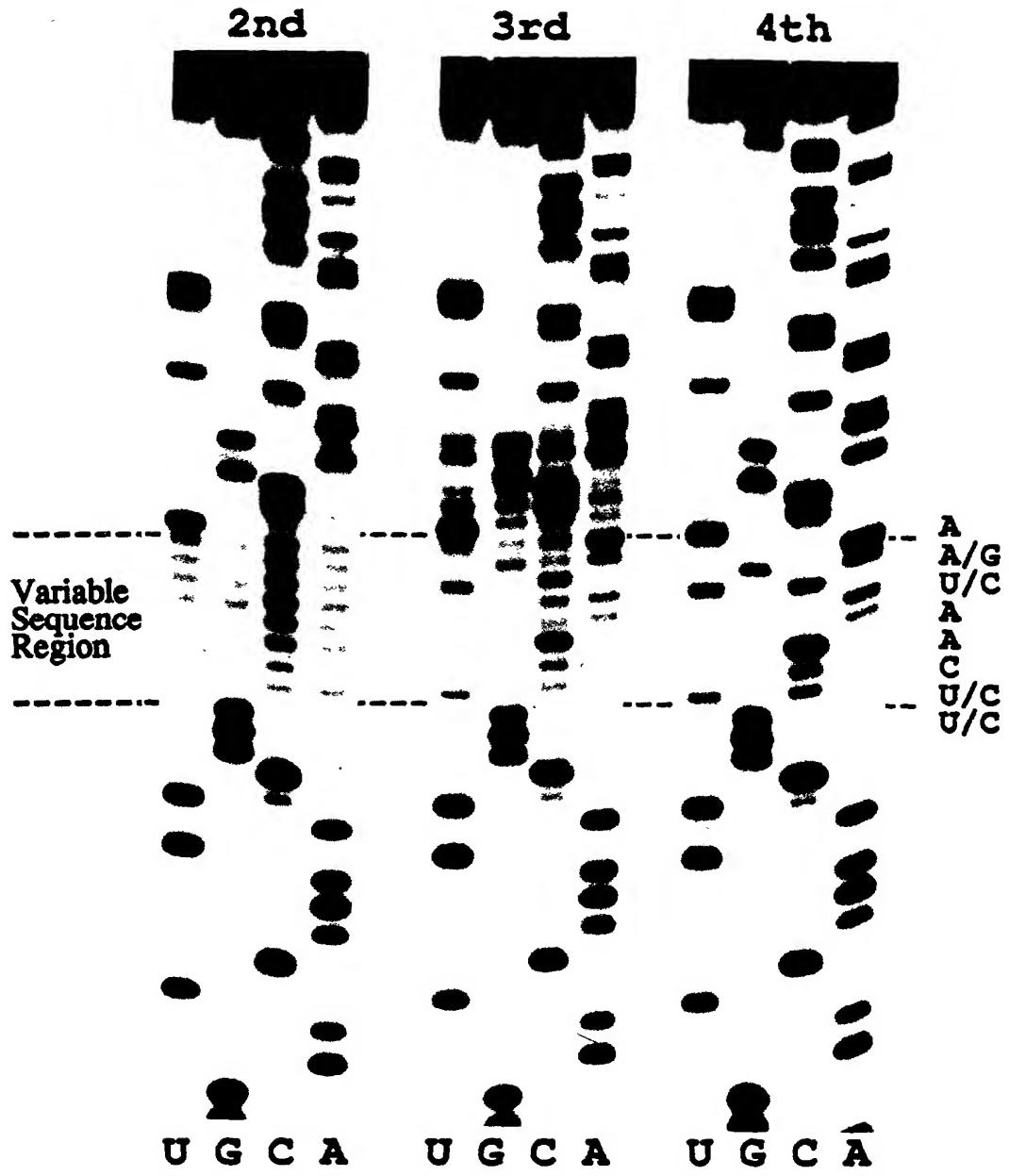


FIG. 4

EXPERIMENT:

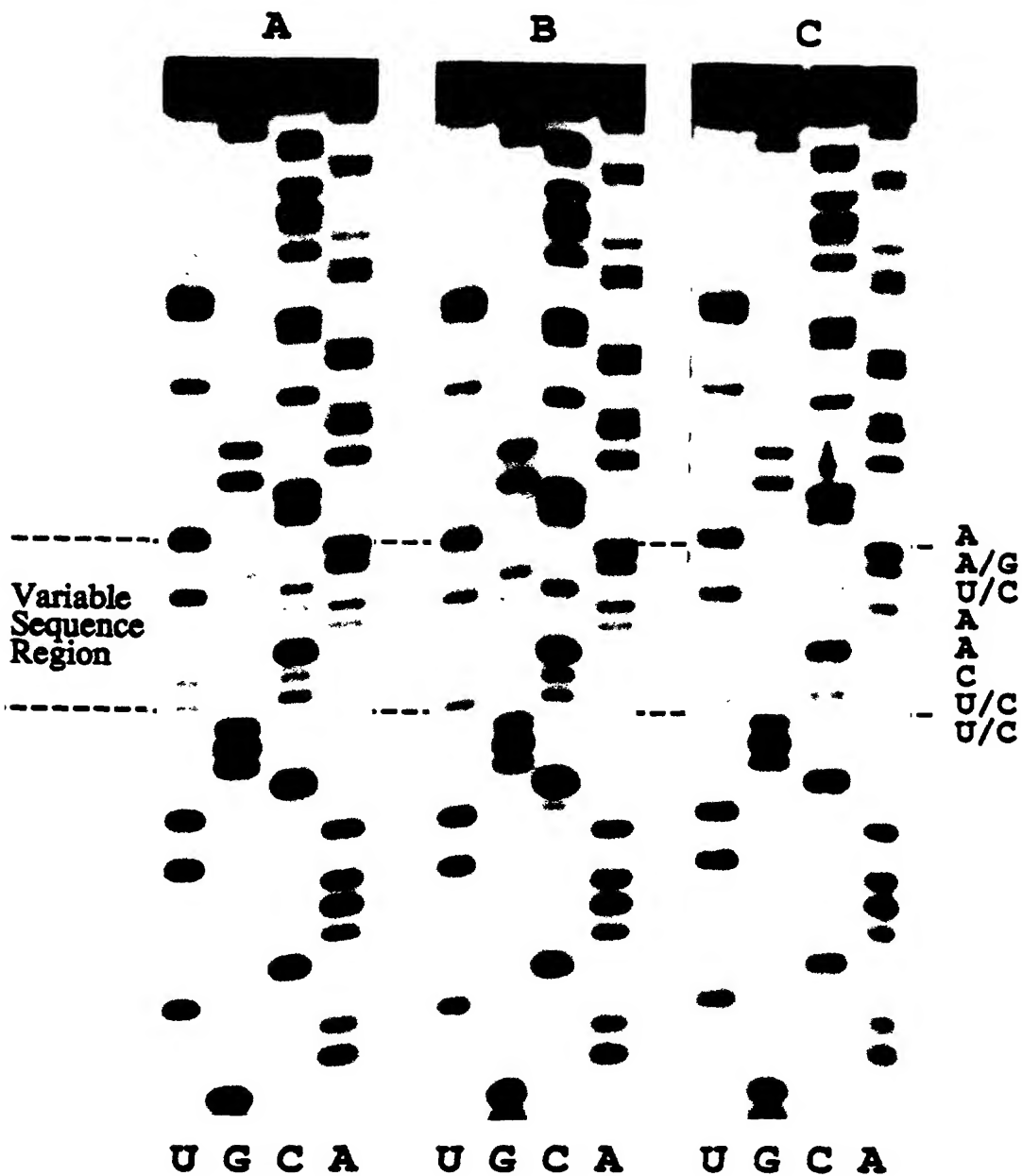


FIG. 5

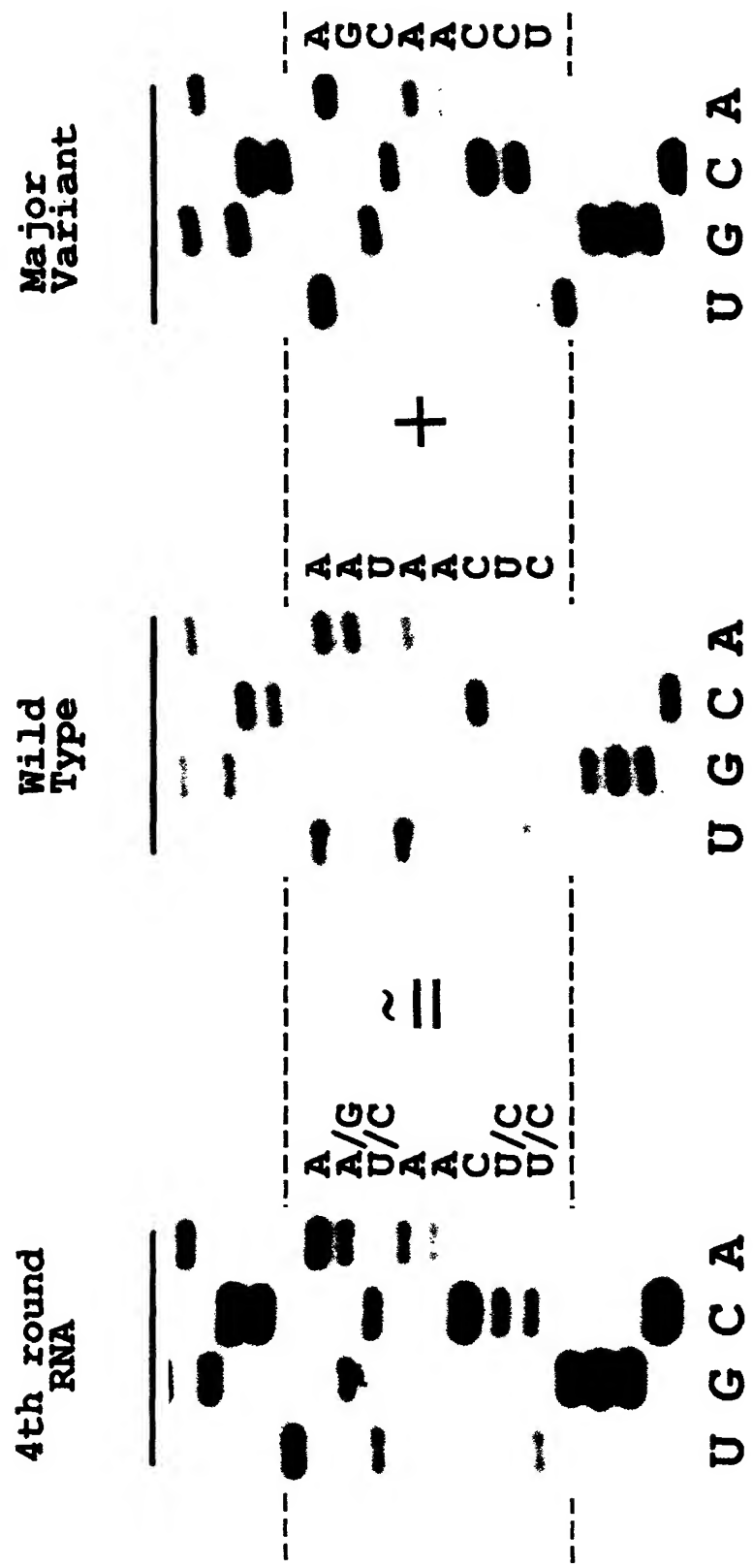
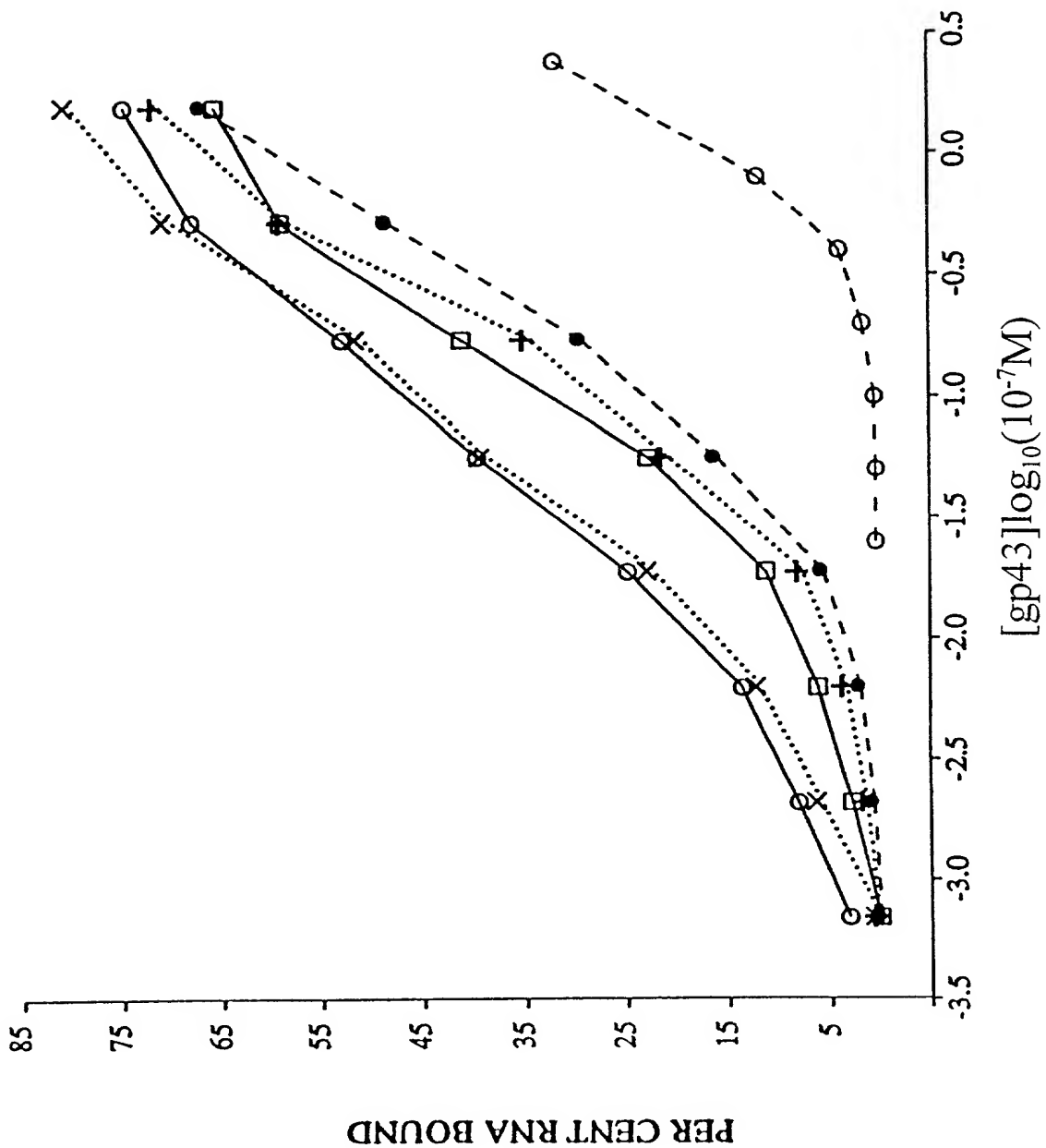
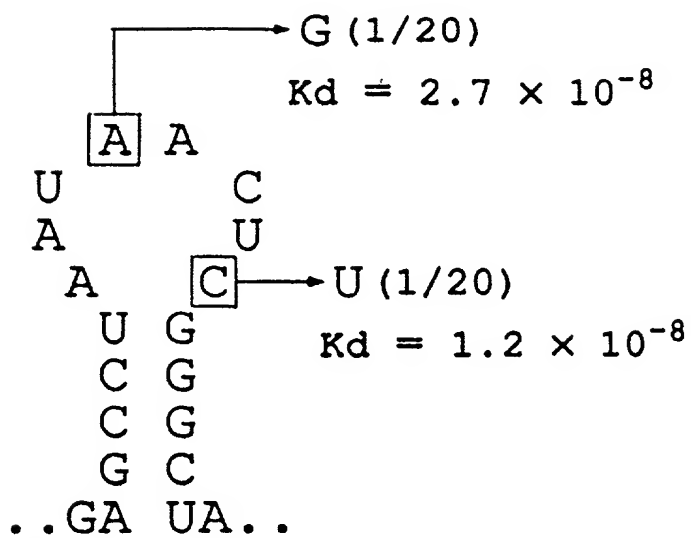
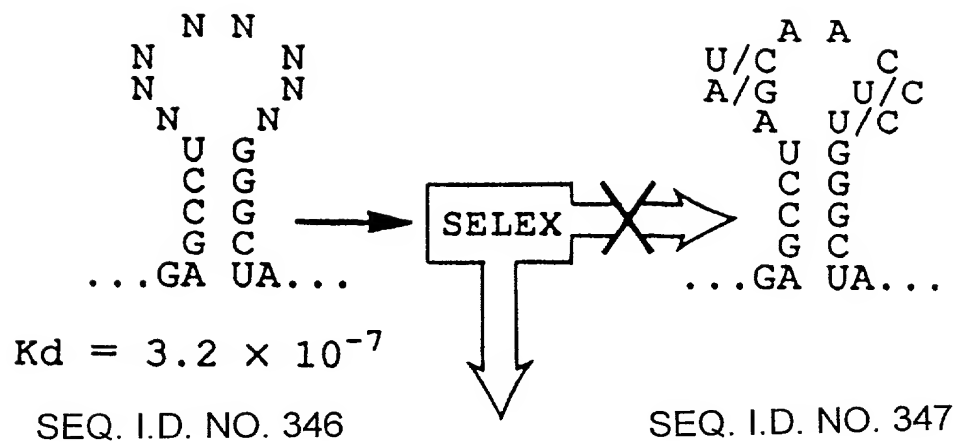


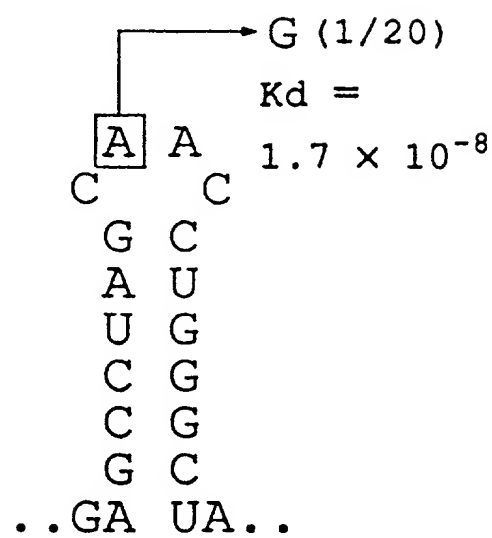
FIG. 6





Wild Type
 (9/20)

SEQ. I.D. NO. 348



Major Variant
 (8/20)

SEQ. I.D. NO. 349

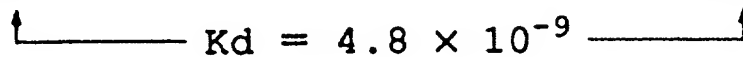


FIG. 7

VARIABLE TEMPLATE SYNTHESIS USING TERMINAL TRANSFERASE

5' PRIMER
 (OR PRIMARY LIGAND SEQUENCE)
 5' ————— 3' 3' ————— 5' PRIMER

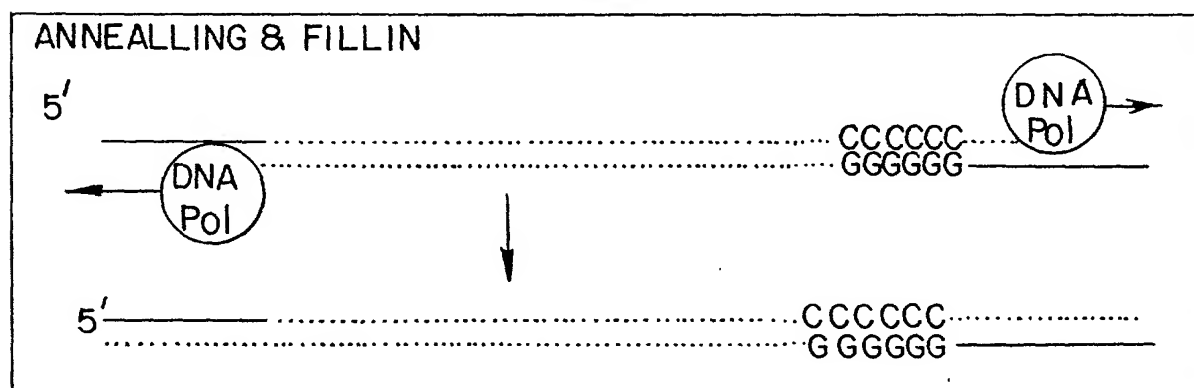
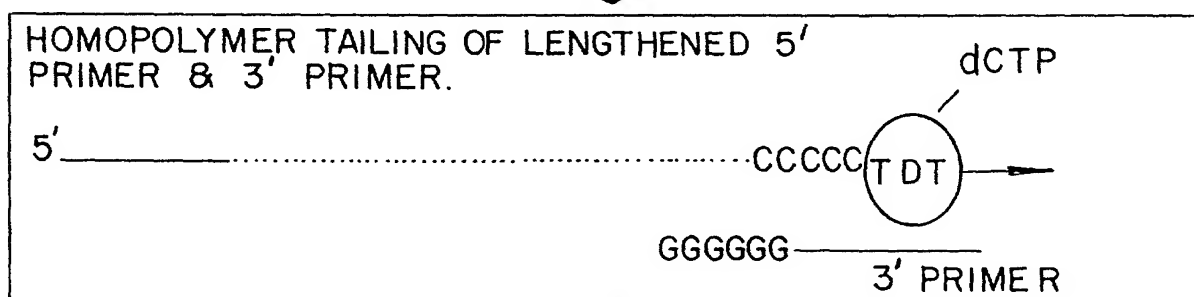
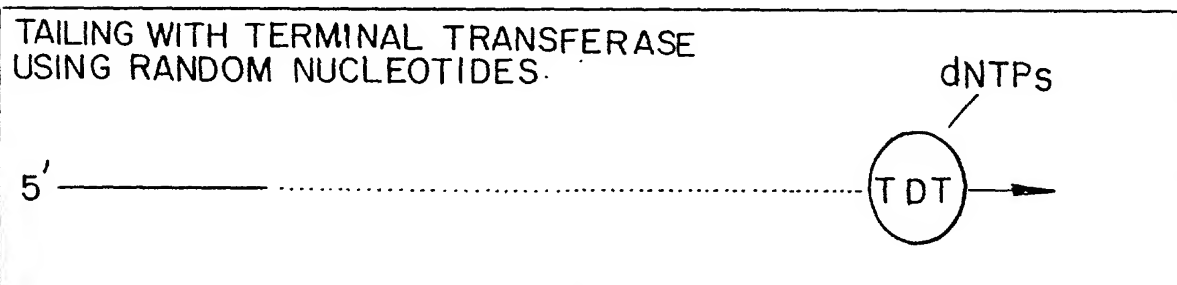


FIG. 8

"WALKING" BY EXTENDING THE PRIMARY LIGAND.

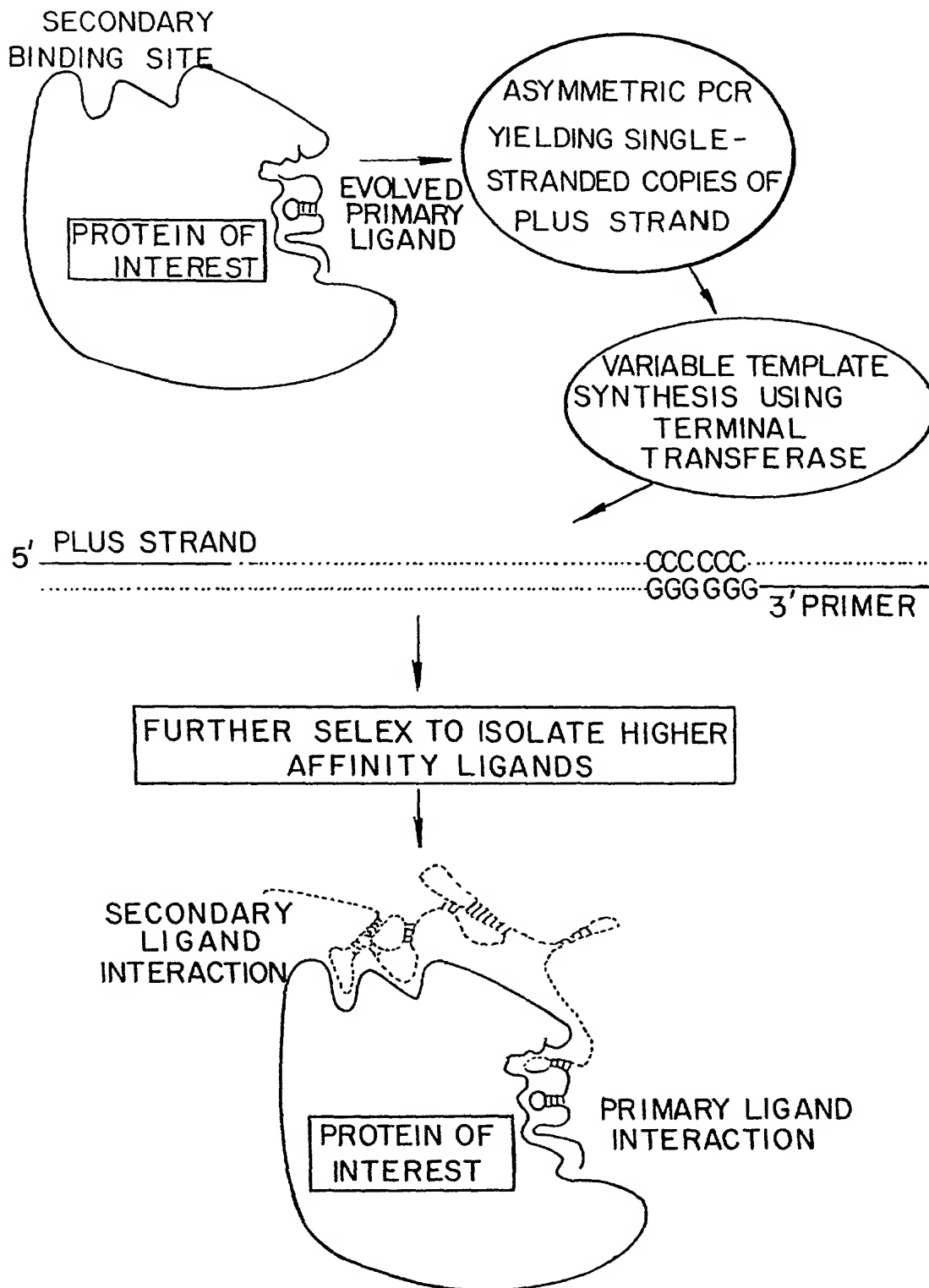


FIG.9

ANCHORING OF BRIDGING OLIGONUCLEOTIDE &
SECONDARY LIGAND EVOLUTION.

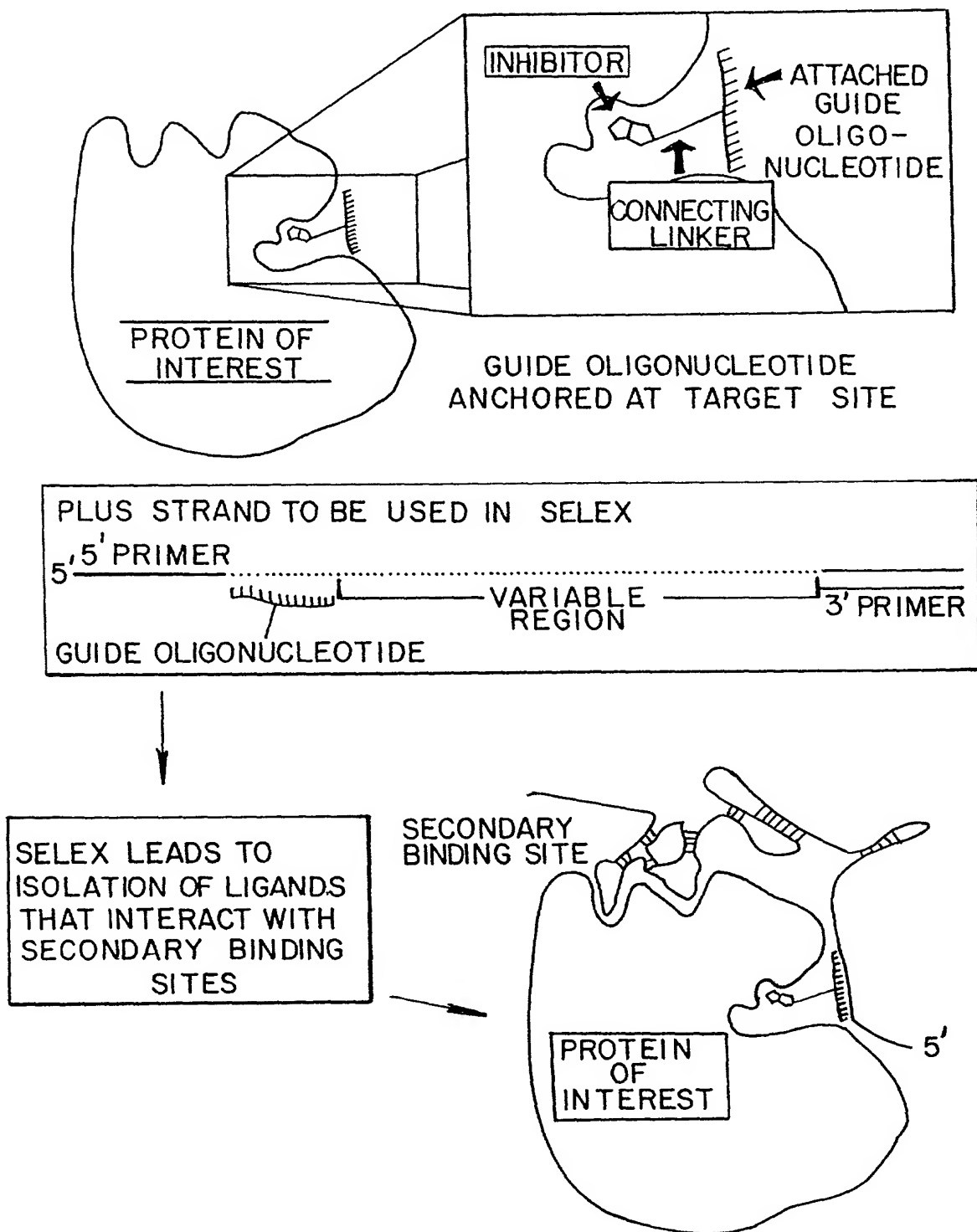


FIG.10

SECONDARY LIGAND-DIRECTED PRIMARY LIGAND EVOLUTION.

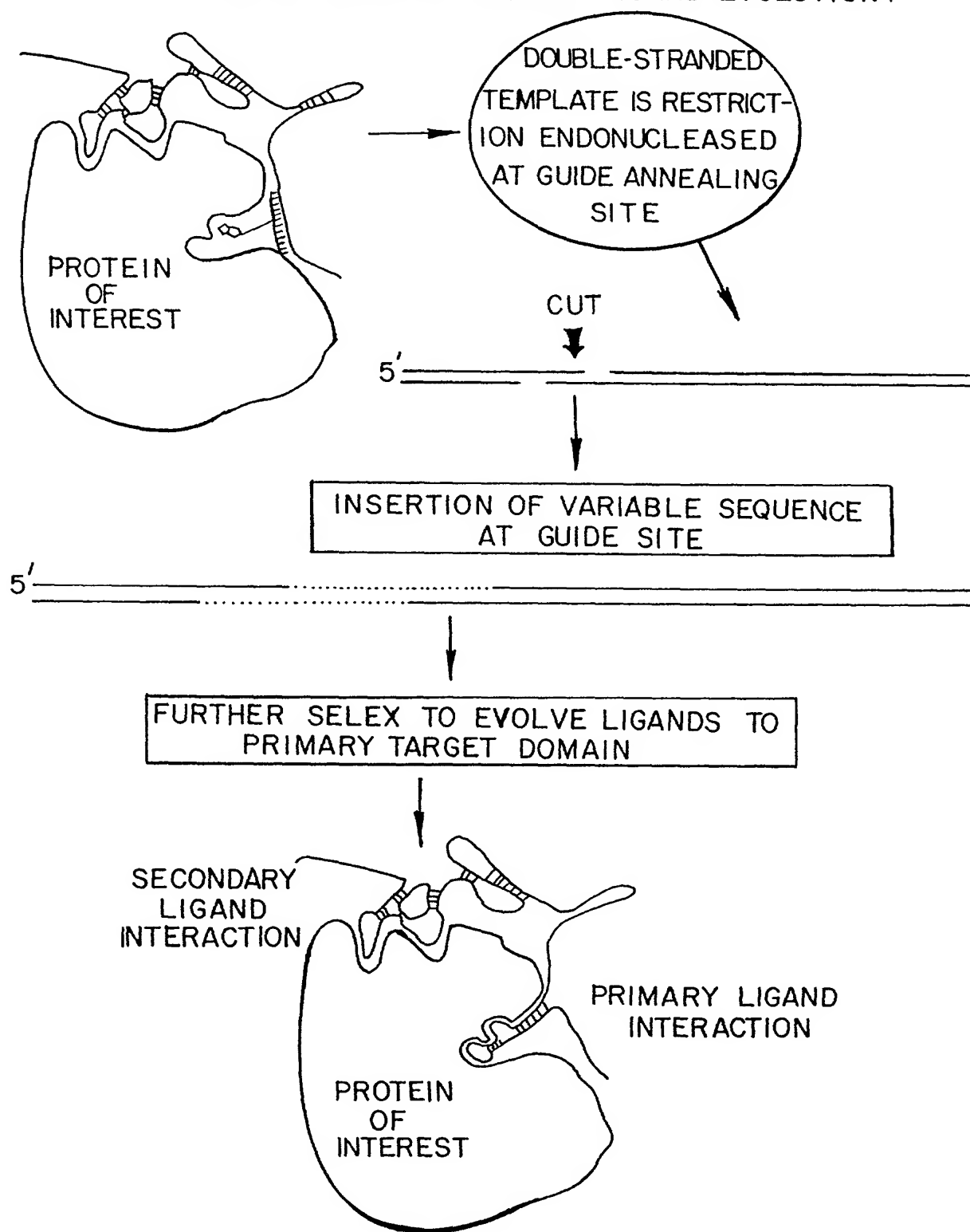
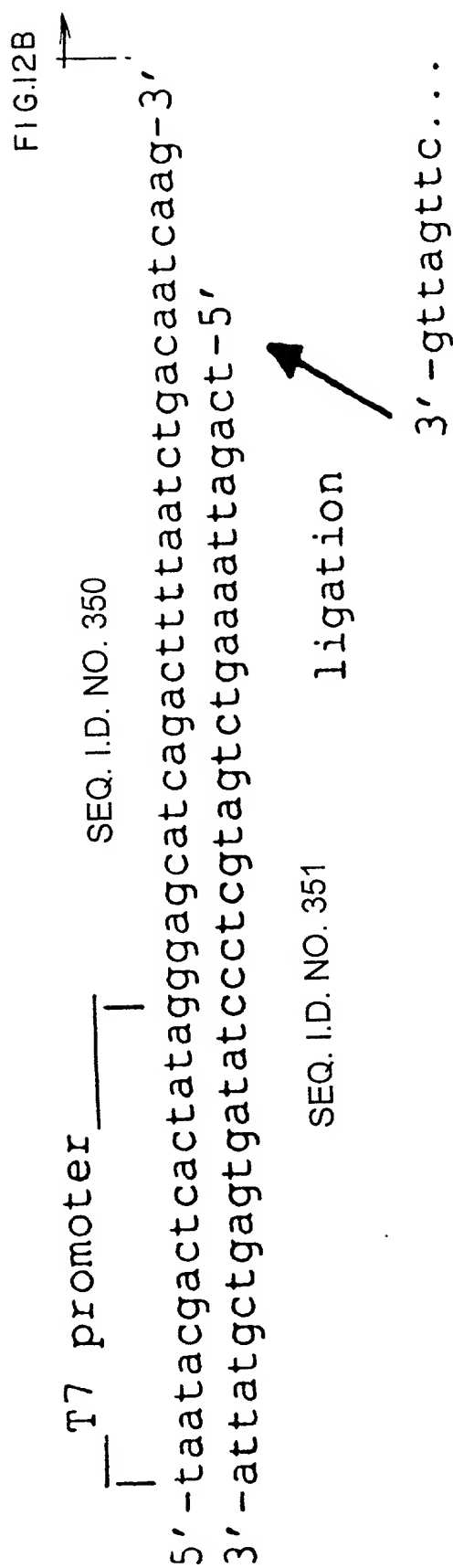


FIG. 11

10037986-101601



in vitro transcript



FIG.12 A

TTTTT" 986/600T

← 12A

5'-atctatgaaagaattttatatctc-3'

3'-cttaaaatatagagataaactttgcctaggcc-5'



ligation

SEQ. I.D. NO. 352

32n...tagatacttt-5'

SEQ. I.D. NO. 353

uuauaucucuauugaaacggaucgg-3'

← 12A

SEQ. I.D. NO. 354

FIG. 12B

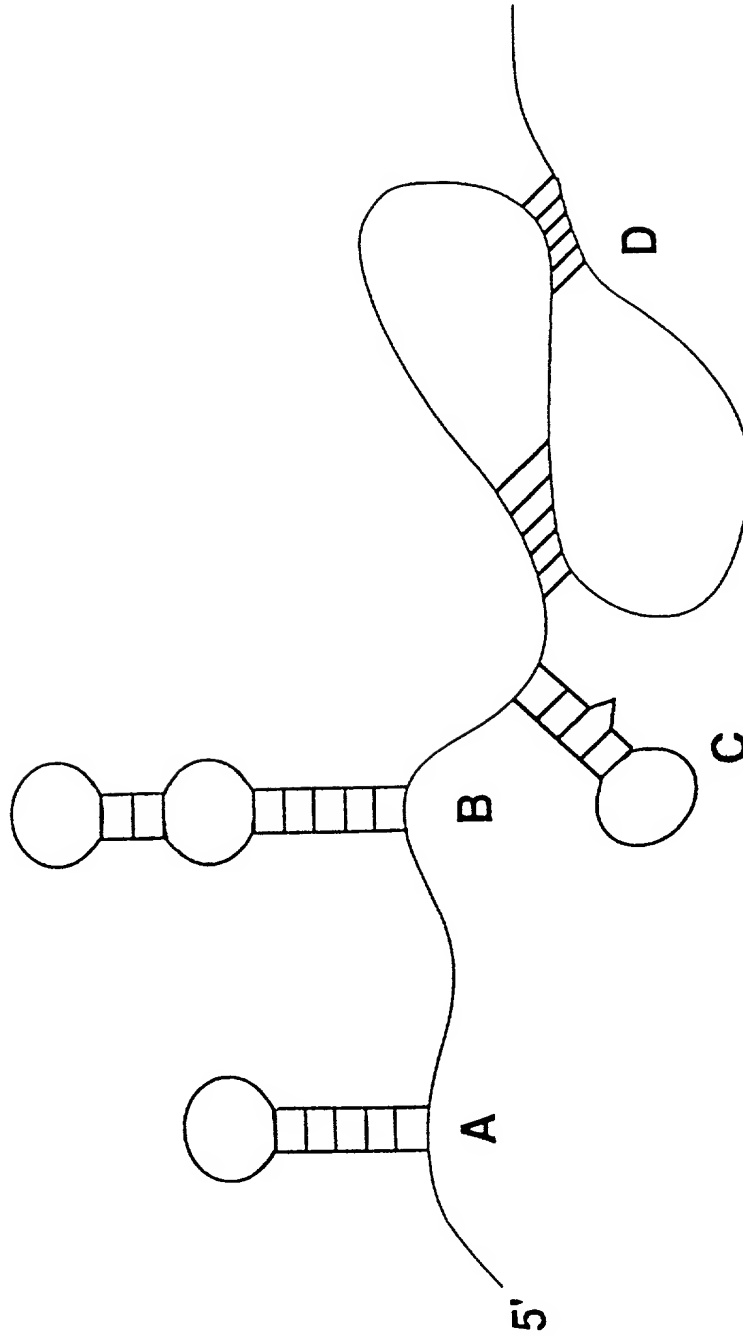
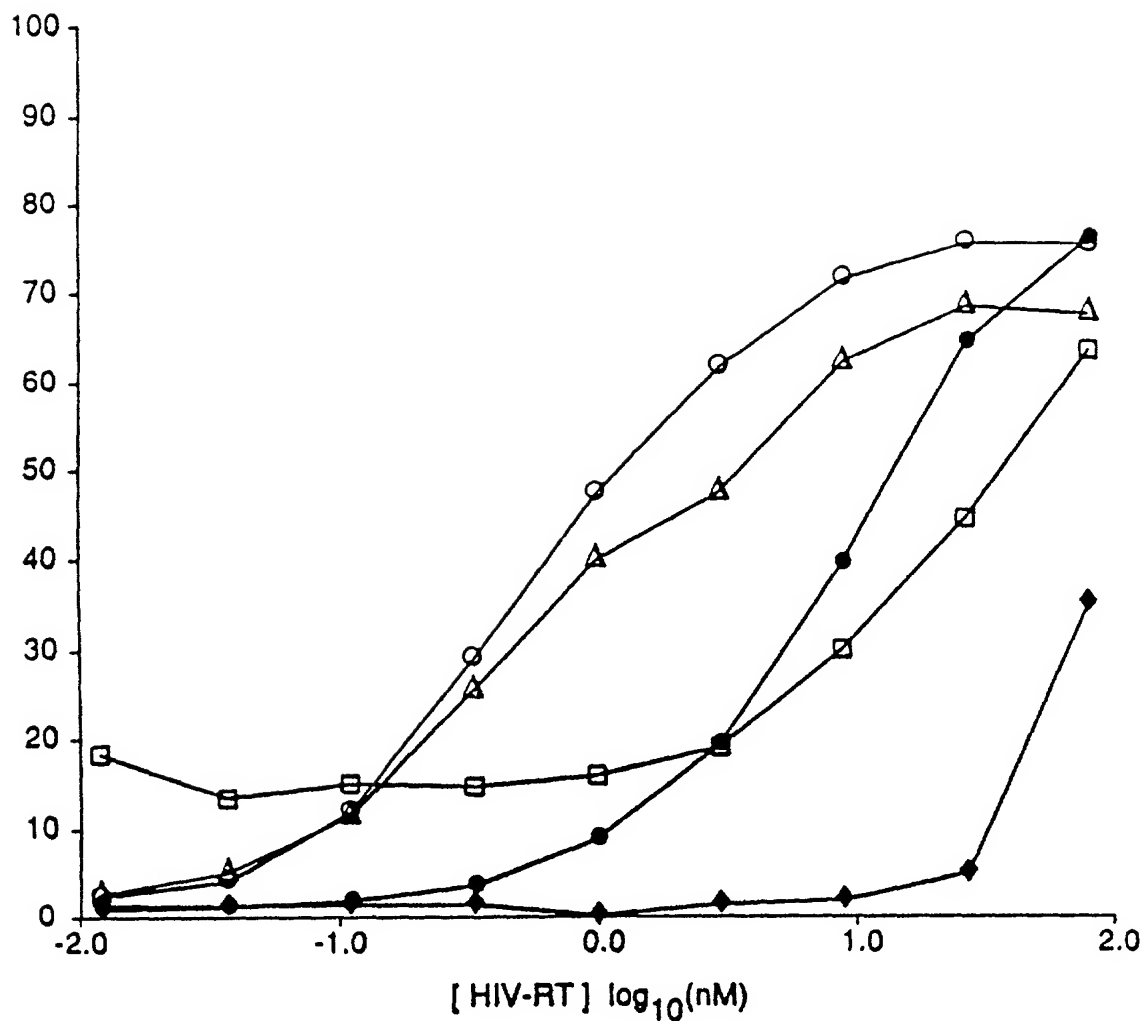


FIG. 13

FIG. 14



Δ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAAACUGAACAaucu (13)

○ 1.3 ucaagAAUAUCUUCCGAAGCCGAACCGGAAAACCGGCaucu (1)

● 1.3 -----G-----A----- (1)

□ 1.4 ucaagGGCAUCUGGGAGGGUAAGGGUAAGGUUGUCGGaucu (4)

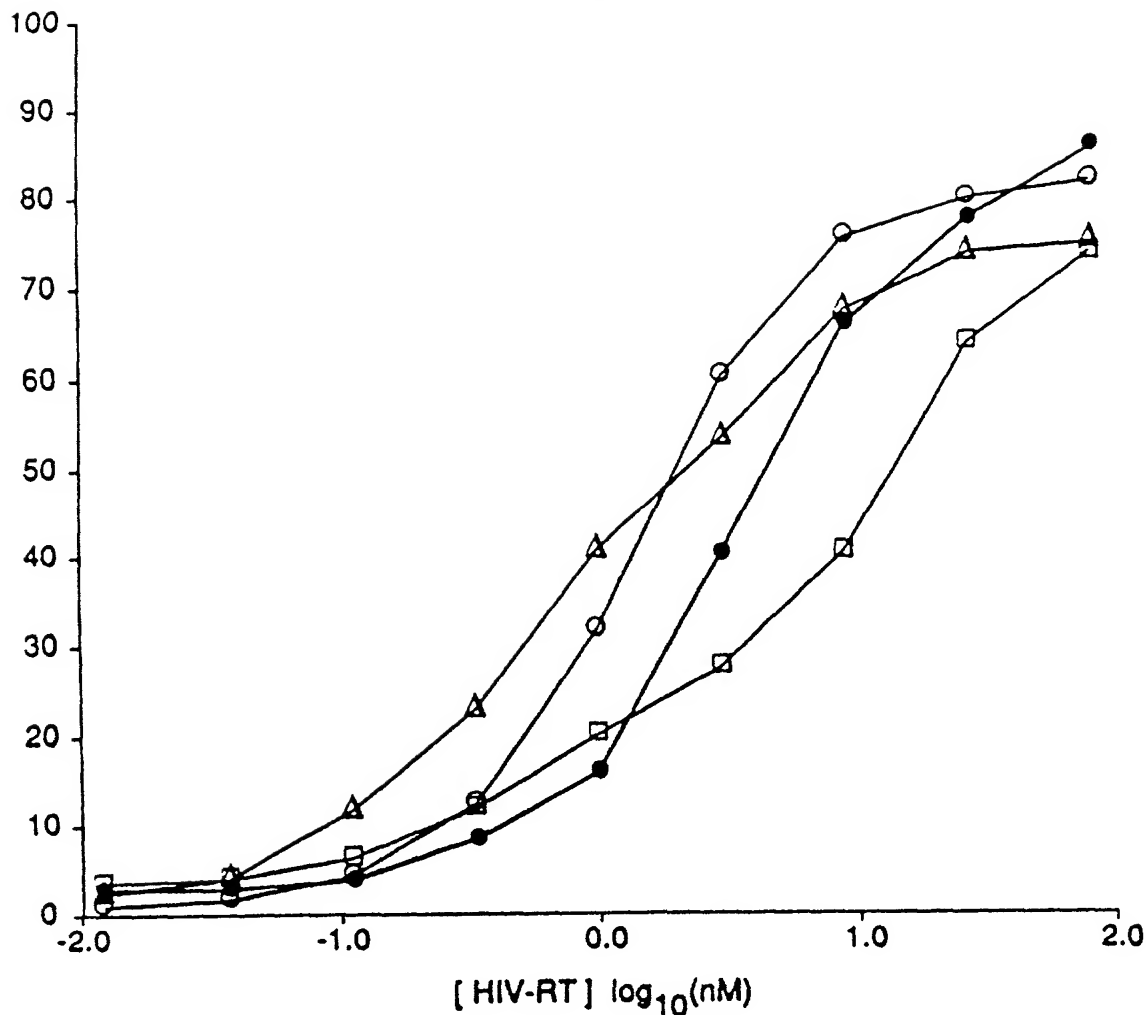
Δ 1.1 = SEQ. I.D. NO. 355

● 1.3 = SEQ. I.D. NO. 357

○ 1.3 = SEQ. I.D. NO. 356

□ 1.4 = SEQ. I.D. NO. 358

FIG. 15



ISOLATE

○ 2.1a ucaag--AAUAUA-UCCGAACUCGACGGGAUAACGAGAA-Gaucu (3)

□ 2.2b ucaagUACCUAGGUGAUAAAAGGGAGAACACGUGUGa-cu (13)

● 2.5b ucaagACAGUAUCCGUUCUUGAUCAUCGGGACAAAUGaucu (3)

△ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAAACUGAACAAUcu (13)

○ 2.1a = SEQ. I.D. NO. 359

● 2.5b = SEQ. I.D. NO. 361

□ 2.2b = SEQ. I.D. NO. 360

△ 1.1 = SEQ. I.D. NO. 362

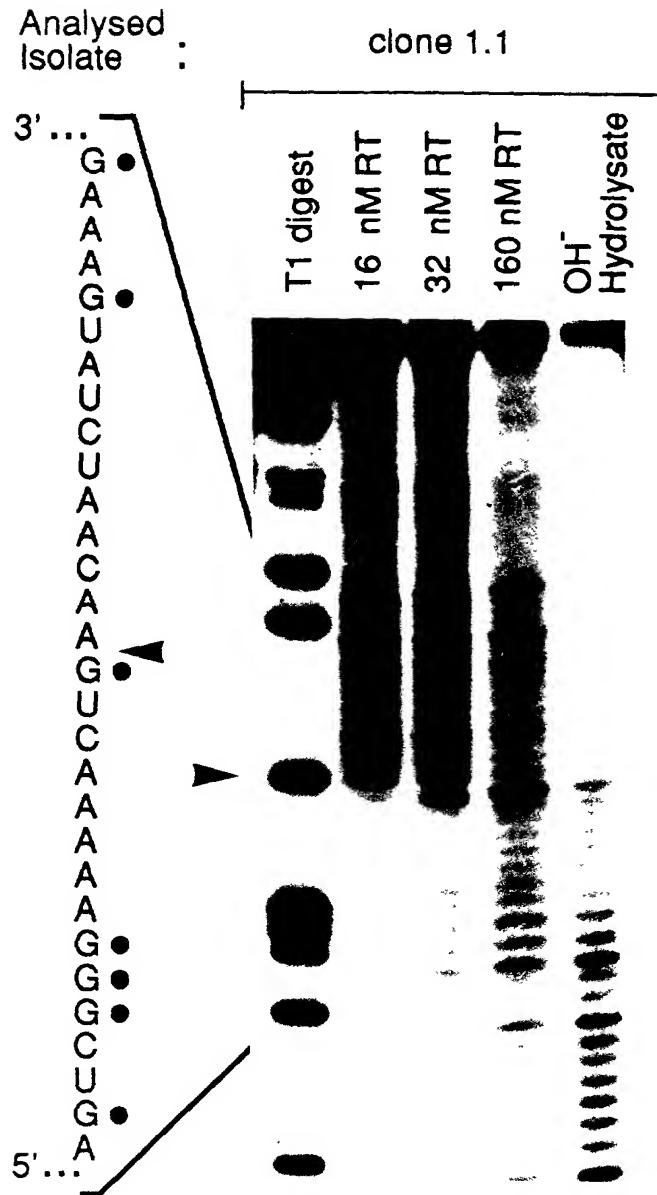


FIG. 16 A

SEQ. I.D. NO. 363

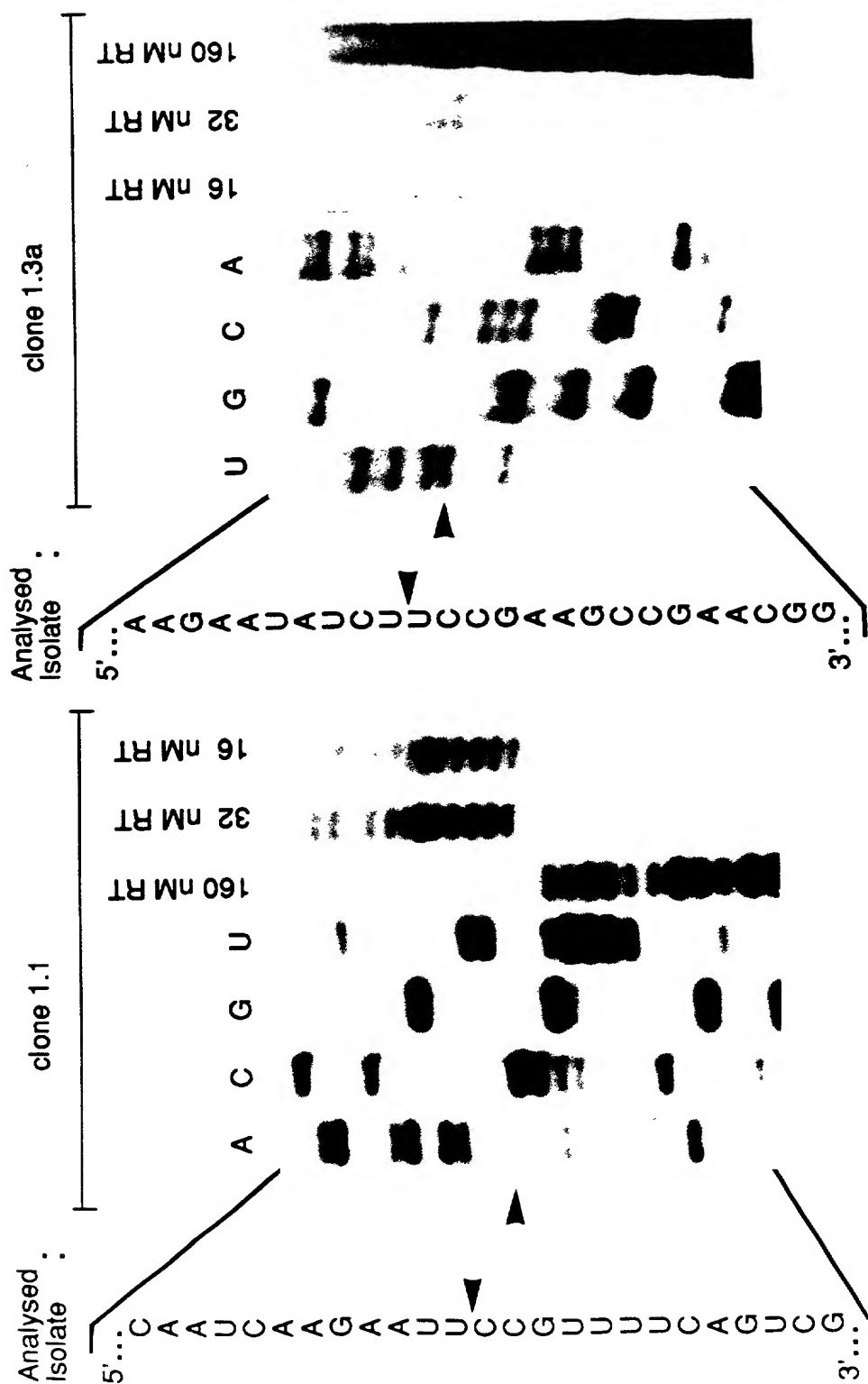
10037985-701801



FIG.16 B

SEQ. I.D. NO. 364

FIG. 16 C



SEQ. I.D. NO. 366

SEQ. I.D. NO. 365

FIG. 17B

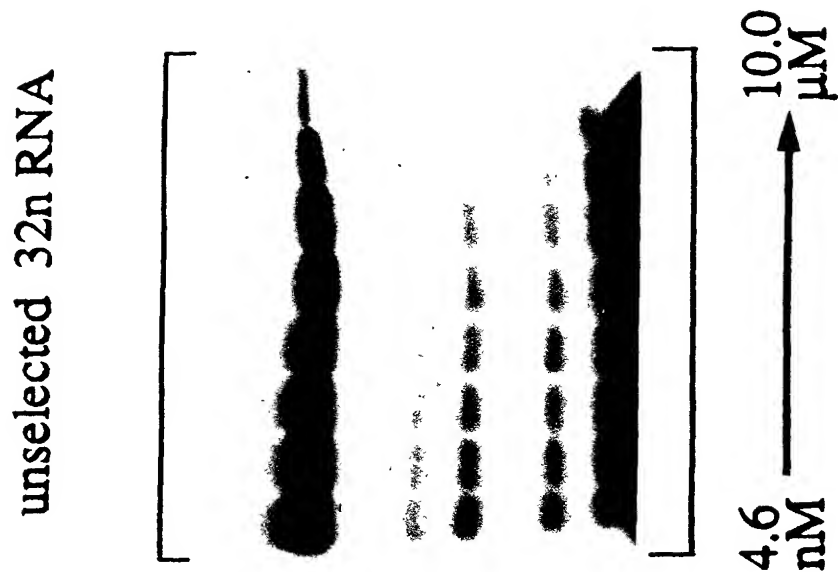


FIG. 17A

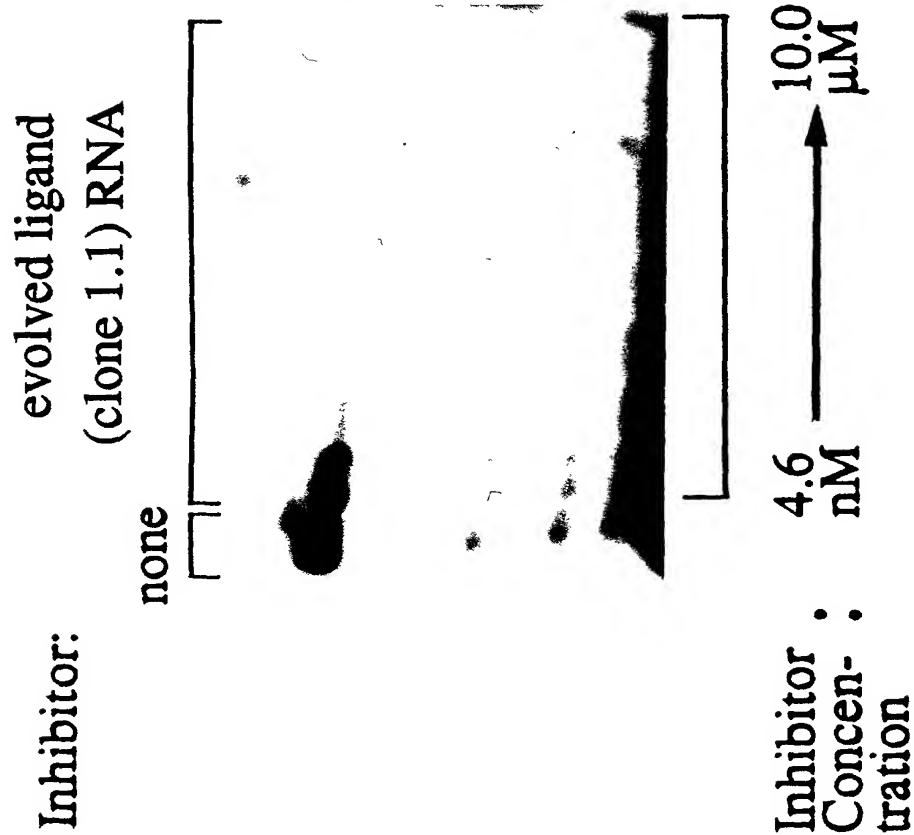


FIG. 18

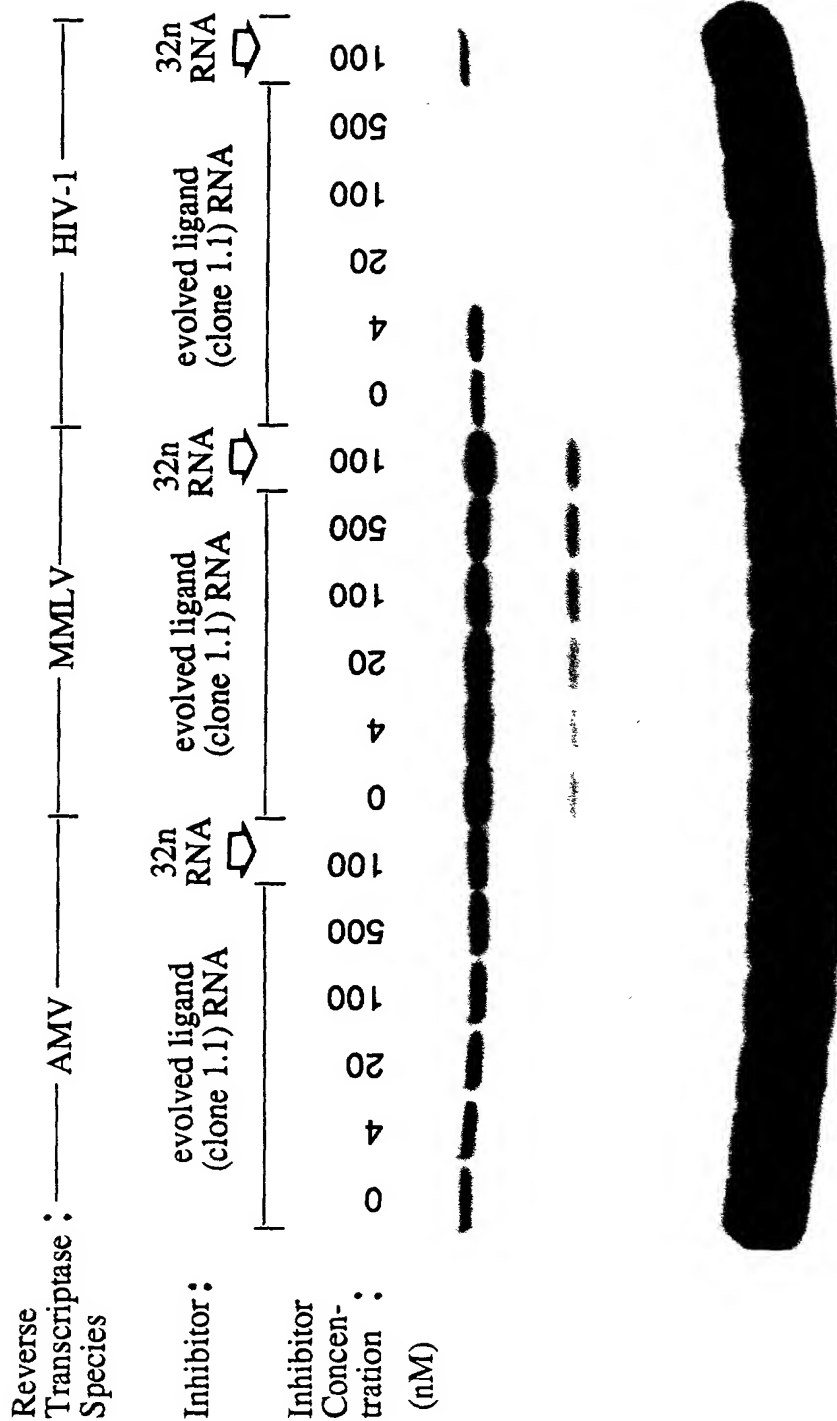
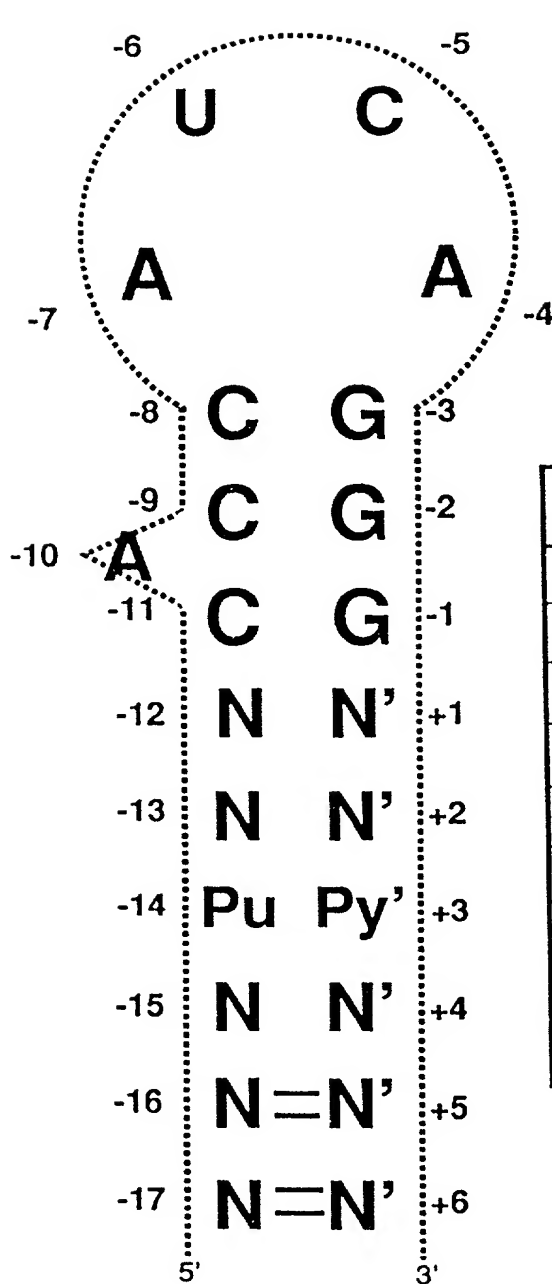


FIG.19B



	A	C	G	U
-4	36	0	0	0
-5	0	36	0	0
-6	4	3	1	28
-7	36	0	0	0
-10	36	0	0	0

	AU	CG	UA	GC	UG	GU	Budge	END
-8/-3	0	24	0	12	0	0	0	0
-9/-2	0	25	0	10	1	0		
-11/-1	0	24	2	10	0	0	36	0
-12/+1	8	1	8	10	7	1	0	1
-13/+2	6	5	8	9	3	1	3	3
-14/+3	9	0	4	10	2	3	3	4
-15/+4	4	0	9	6	0	1	6	8
-16/+5	10	1	2	1	1	3	0	2
-17/+6	0	4	6	1	4	2	1	1

FIG.19C

FIG.19A

SEQ. I.D. NO. 367

FIG.20

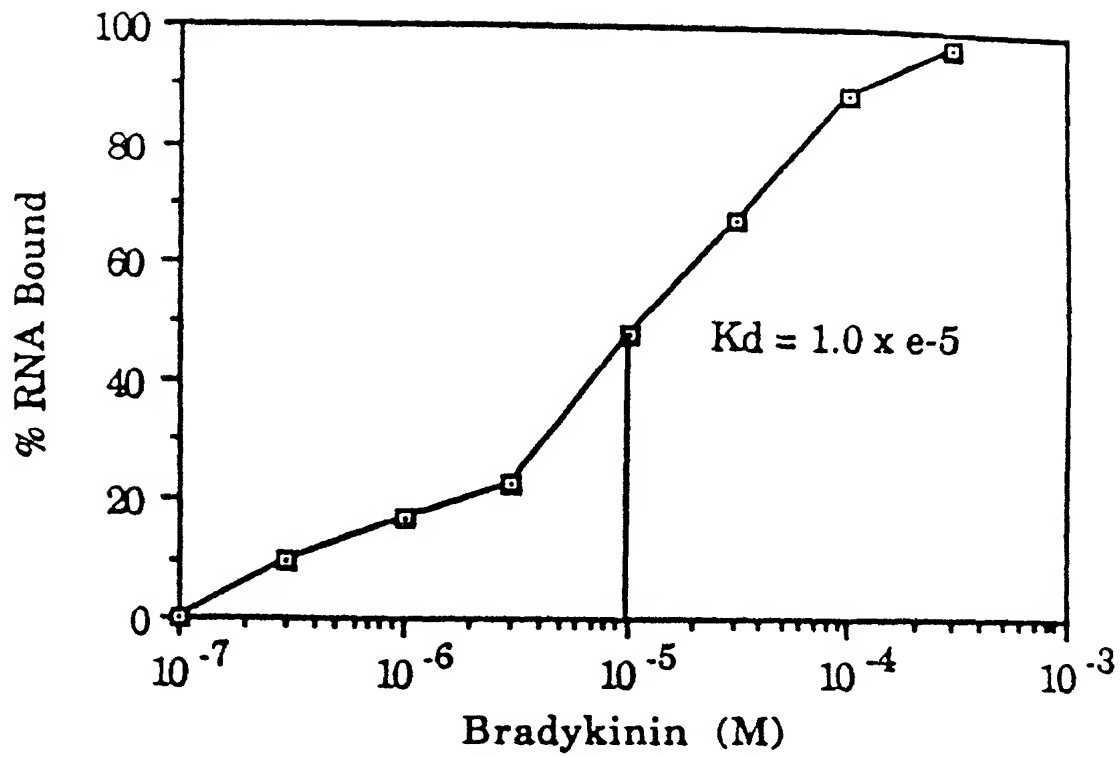


FIG.2IA

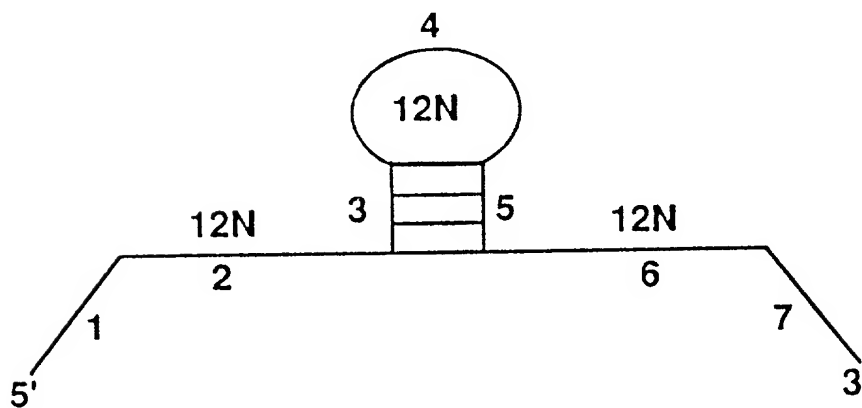
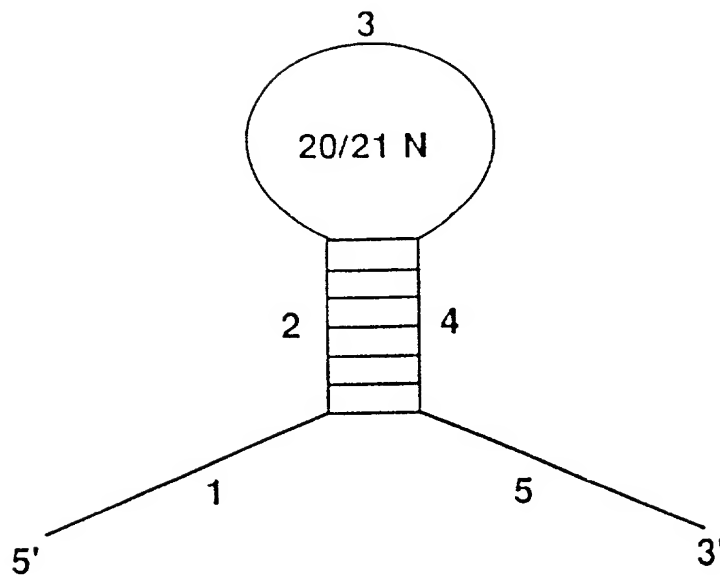


FIG.2IB

FIG. 22

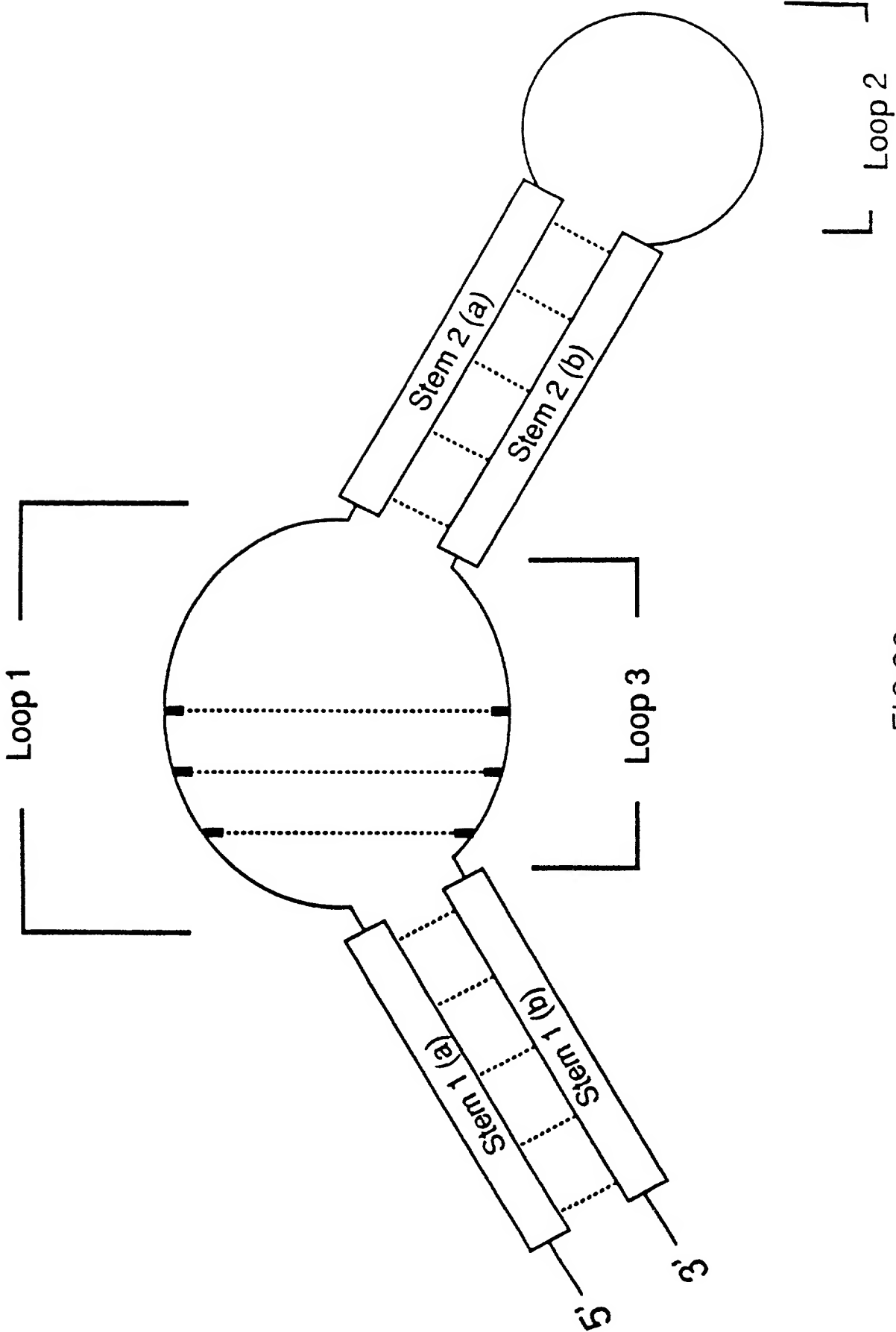


FIG.22

Motif I (6a)

UUGAGAAA G
 5' ...GGUGCA ||| CAC U (NUCLEOTIDES 2-38 OF SEQ. I.D. NO. 301)
 3' ...ucuaUGU ||| GUG U
 --CUCA-G U

Motif III (9a)

CC UUGaucua-
 A GG ||||| uga-3'
 A CC ||||| GCUU-5'
 UU --CUAGUAA

SEQ. I.D. NO. 369

Motif II (1c)

AAGAUU UCU
 5' ...AGAUG CAGC
 3' ...ucuaC GUCC A
 -ACA-G UAG

SEQ. I.D. NO. 368

WT (Motif II-like Domain)

U ACGGUA
 A GACGUG || CA.....3'
 CUGCGAC || GU.....5'
 A -GCG-G

SEQ. I.D. NO. 370

FIG. 23

FOOT-9862E001

FIG. 24

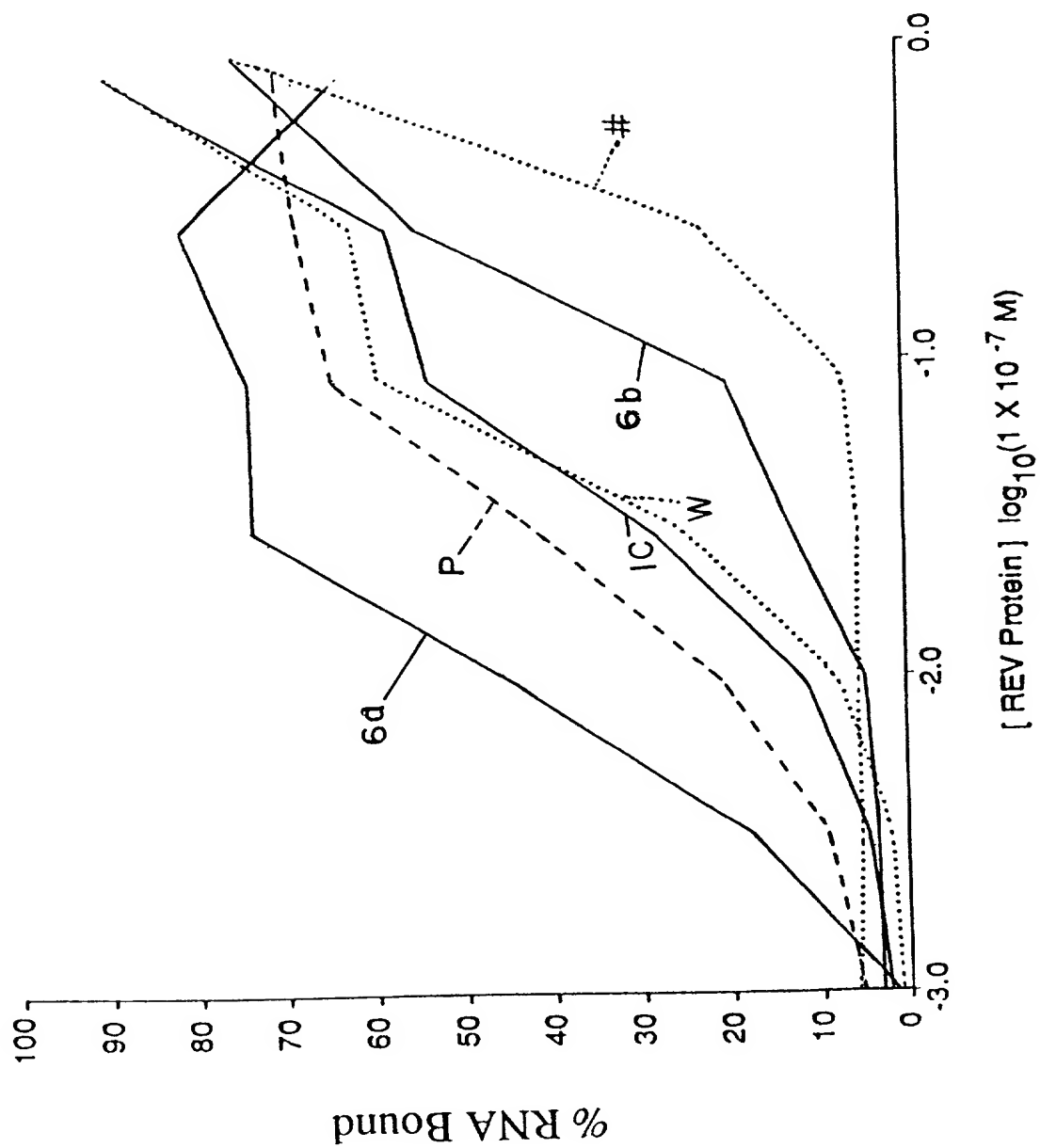


FIG. 25

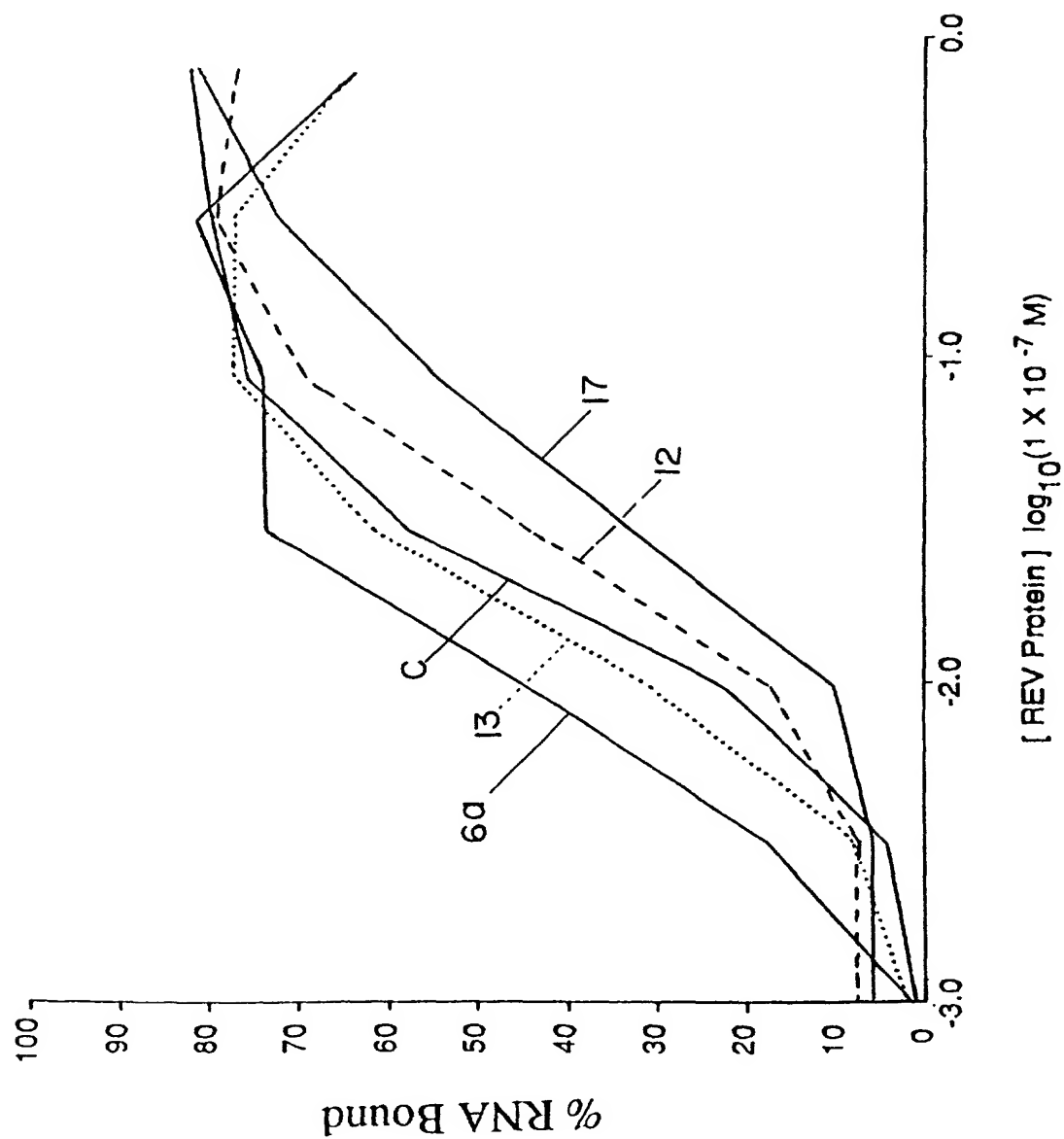
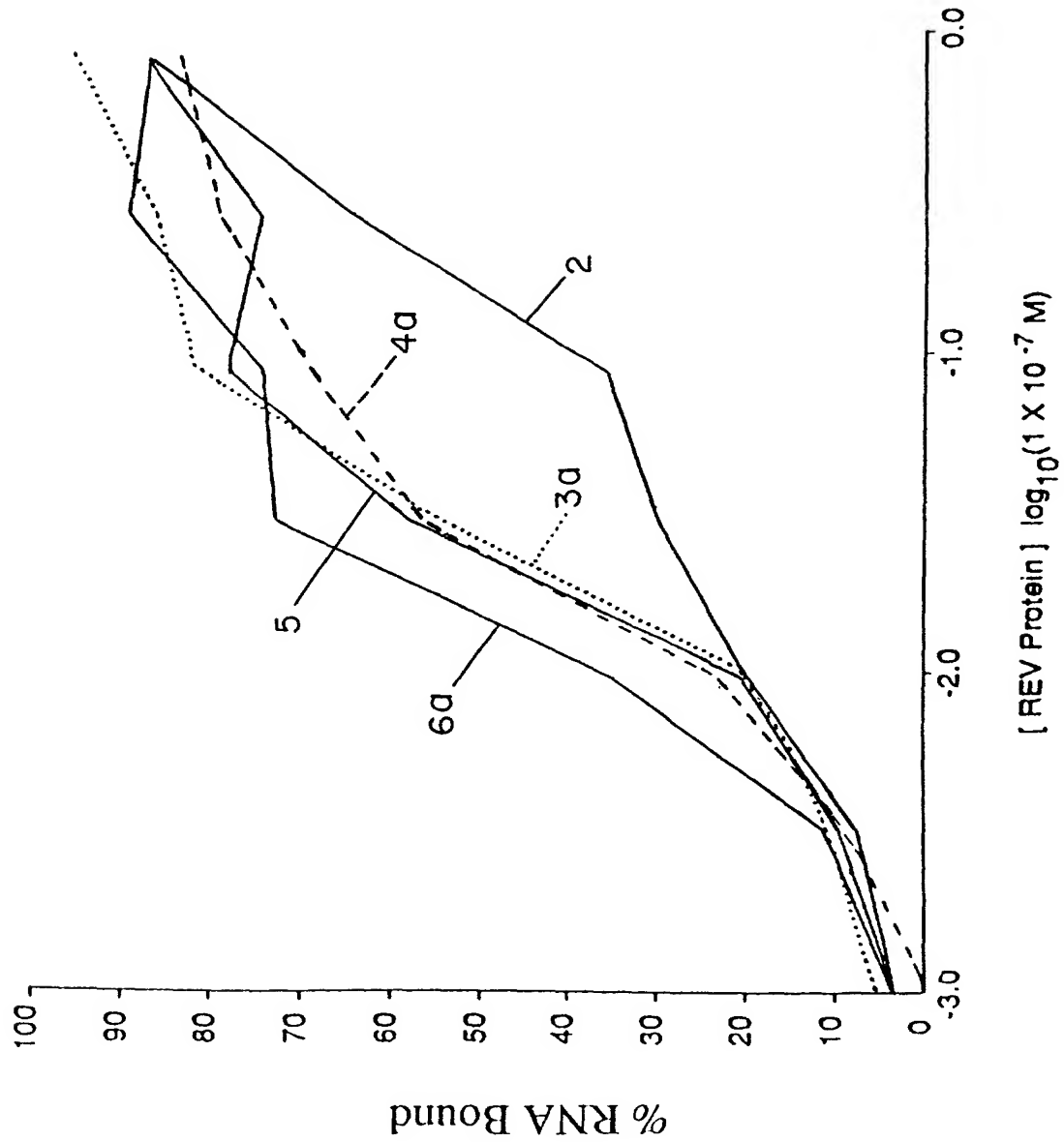


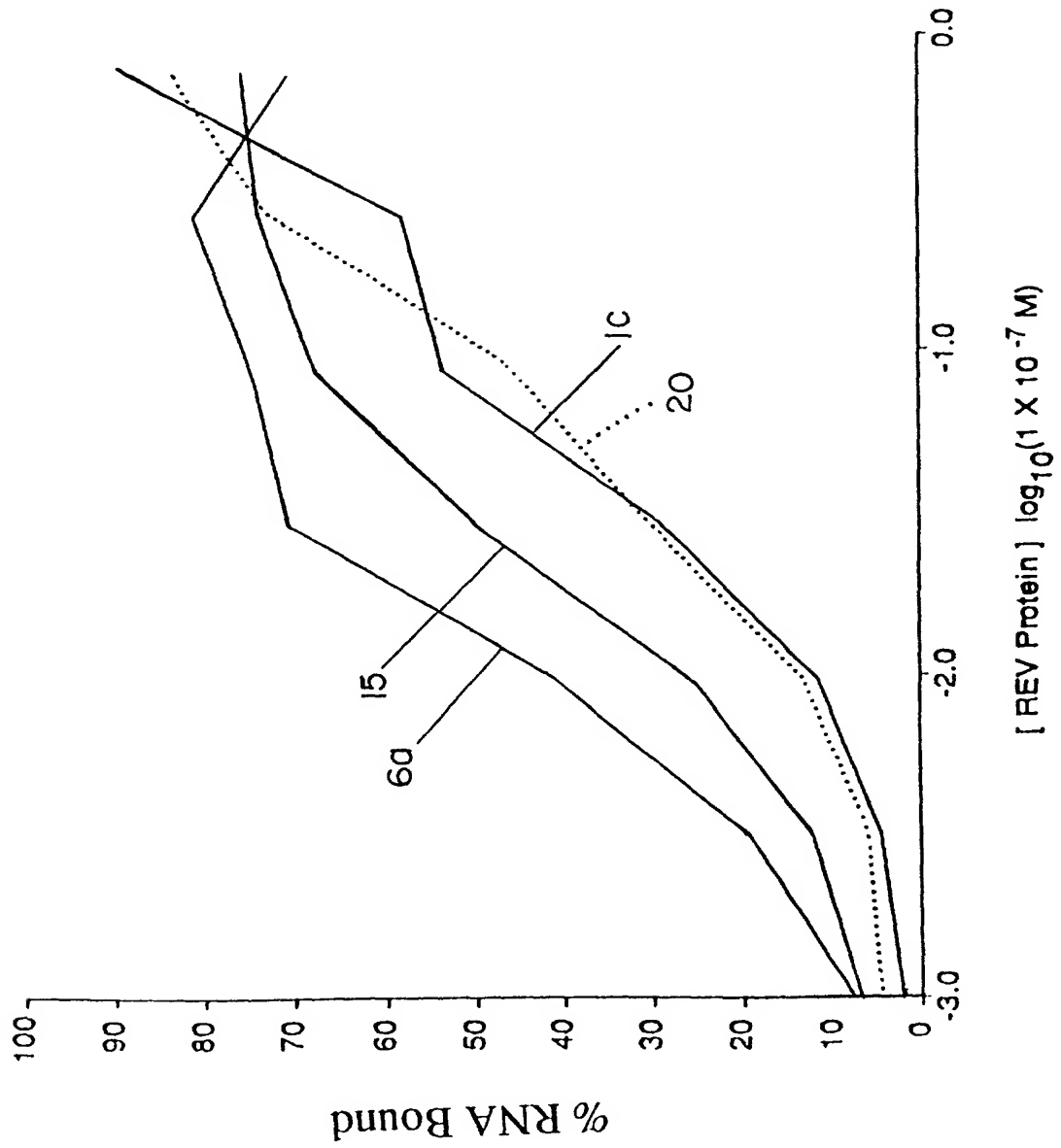
FIG. 26

FIG. 26



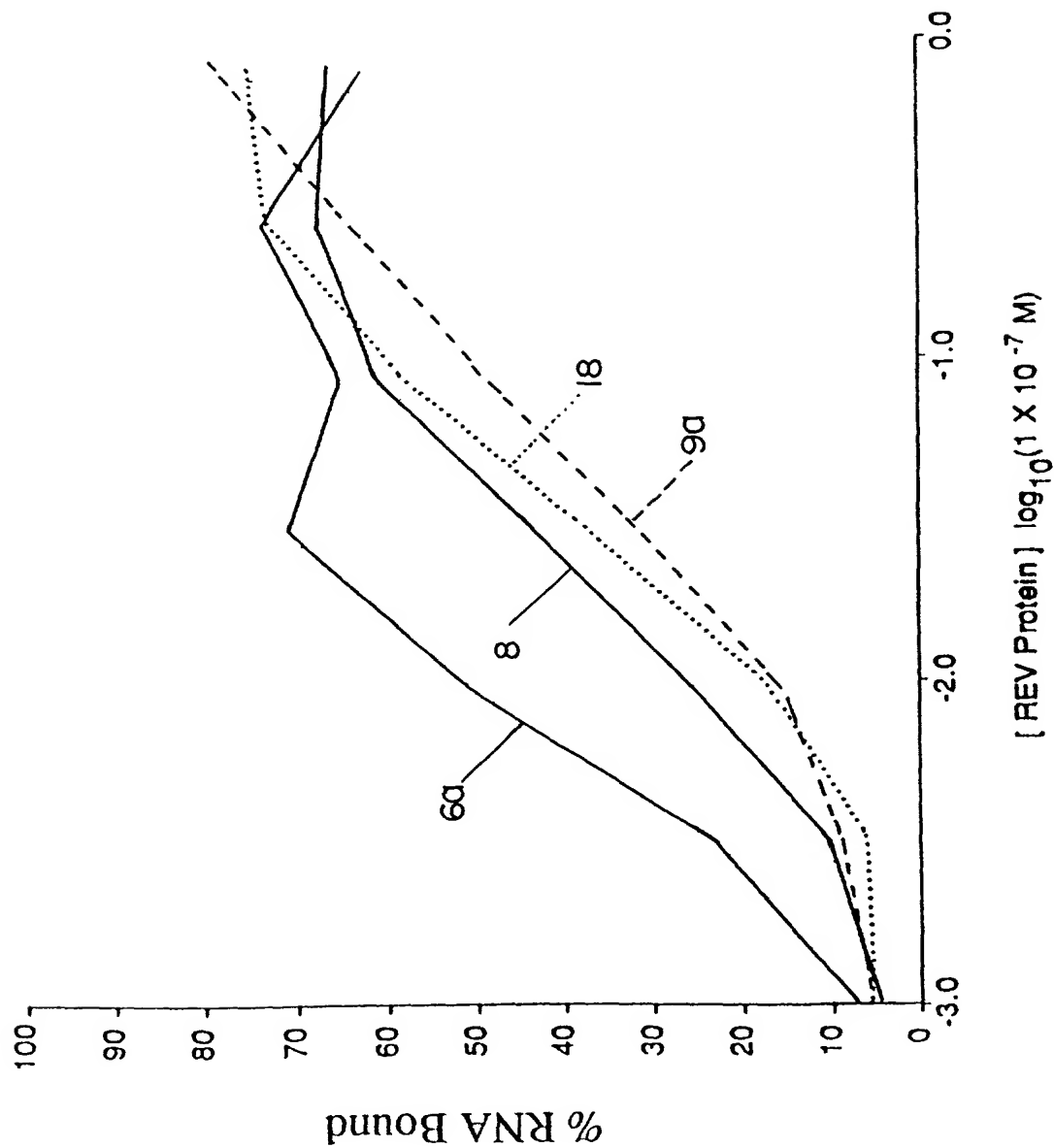
FOOTNOTES

FIG. 27



FOOTNOTES 9864E001

FIG. 28



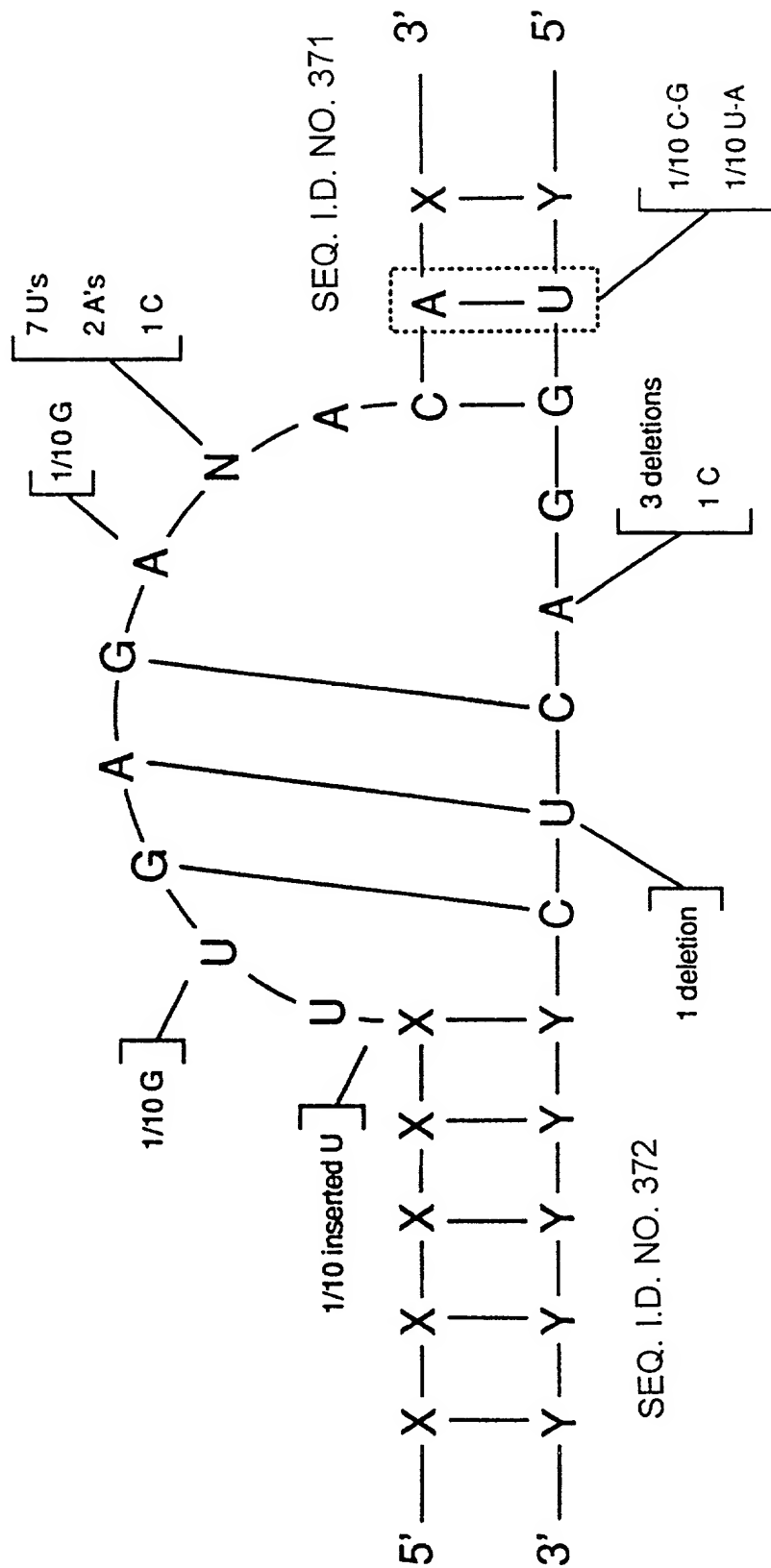
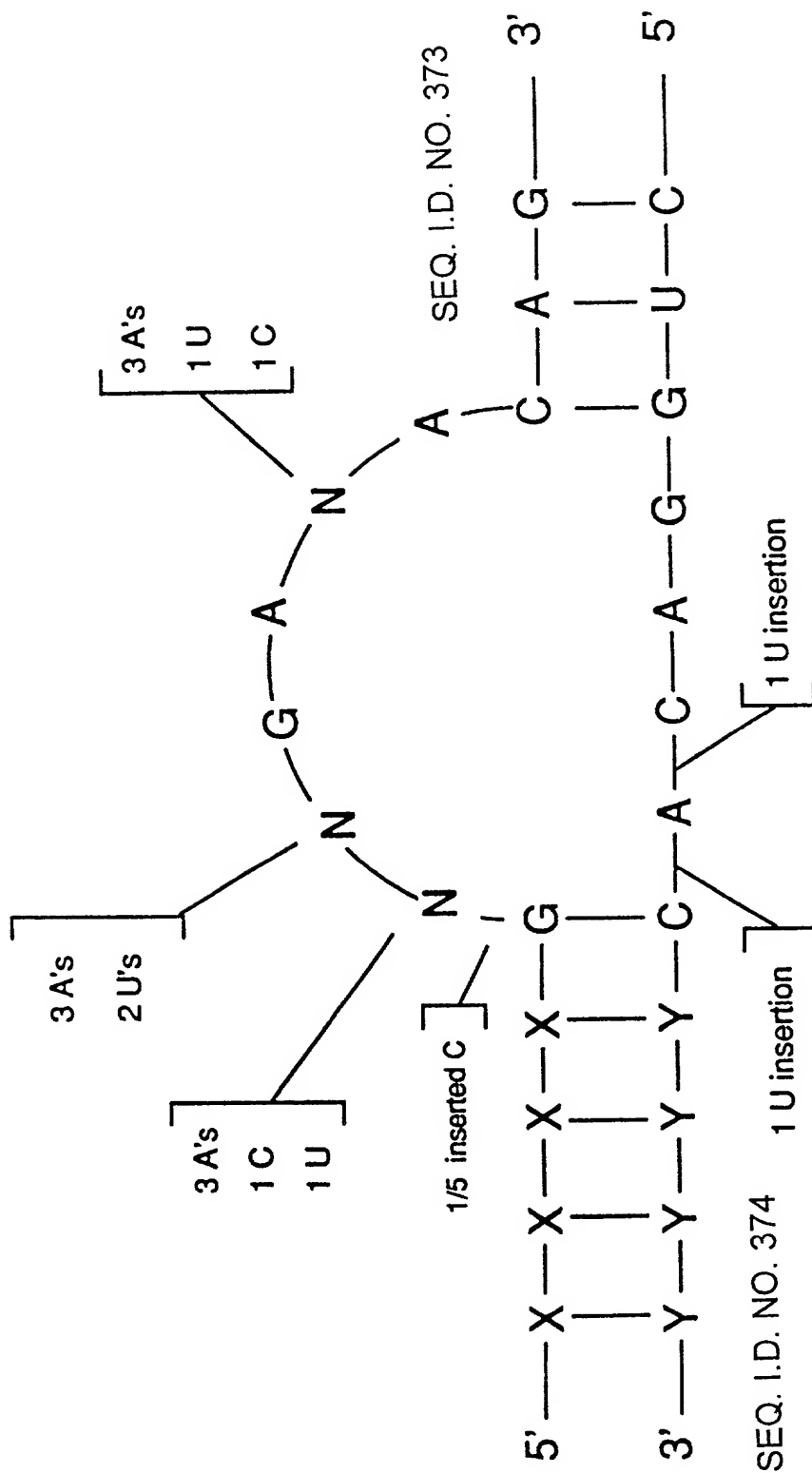


FIG. 29

FIG. 30



Motif II

FIG. 31

